Forage Quality Variation among Maize Inbreds: In Vitro Fiber Digestion Kinetics and Prediction with NIRS

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ABSTRACT

The nutritive value of forage maize (*Zea mays* L.) may be improved through genetic selection for increased rate of fiber digestion or decreased indigestible fiber concentration. To identify sources of genetic variation, 45 maize inbreds were evaluated for in vitro neutral detergent fiber (NDF) digestion kinetic parameters using stem internode tissue harvested at silking during 2 yr. Near infrared reflectance spectroscopy (NIRS) was also used to estimate NDF digestion kinetic parameters. Maize inbreds varied significantly in NDF concentration and digestion kinetic parameters using either conventional in vitro analysis or NIRS predictions. Using NIRS predictions, inbreds varied in NDF concentration from 497 to 662 g kg^{-1} dry matter (DM), rate of NDF digestion ranged from 0.037 to 0.077 h^{-1}, and extent of NDF digestion was 525 to 735 g kg^{-1} NDF. The ranges for NIRS predicted parameters were less than those observed for the calibration data set by conventional analysis. Correspondence between conventional analysis data and NIRS predictions were good, except for lag time. Digestion kinetics calculated from NIRS predicted residues provided more precise predictions of lag time and fractional rate of digestion when compared with observations derived from conventional analyses, than did direct prediction of these kinetic parameters. Correlations between rate of NDF digestion and 18-h NDF digestibility (r = 0.79) or between potential extent of NDF digestion and 96-h NDF digestibility (r = 0.95) were large enough that these two fermentation intervals might substitute for conducting complete digestion kinetic studies with eight to 10 fermentation times. The substantial genetic variation among these maize inbreds shows good potential for development of silage hybrids with improved fiber digestion parameters. Year and year × genotype interactions were significant suggesting that identification of superior inbred lines will require evaluations in multiple environments.

Use of maize silage by ruminant livestock may be improved through genetic selection for decreased fiber concentration or increased rate or extent of fiber digestion (Jung and Allen, 1995). Decreasing fiber concentrations of forages can increase dry matter intake (Mertens, 1973; Waldo, 1985) and increasing fiber digestibility of maize can increase dry matter intake and rate of gain for steers (Roth and Klopfenstein, 1987). Theoretical models have also shown that increasing fiber digestion rate may improve fiber digestibility by permitting a greater extent of digestion before particles pass from the rumen (Allen and Mertens, 1987).

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Because grain is highly digestible, maize hybrids for silage production are generally chosen based on their grain yield. However, the stalk portion of the maize plant contains 50% or more of the whole plant biomass and most of the fiber, which is much less digestible than fiber in grain (Hunt et al., 1992). For these reasons the stalk is the plant structure most commonly identified as a potential target for genetic improvement. Genetic variation for fiber concentration and dry matter digestibility of maize stalks was observed by Albrecht et al. (1986), Dhillon et al. (1990), and Hunt et al. (1992), and decreases in fiber concentration are commonly correlated with increased digestibility (Dhillon et al., 1990; Hunt et al., 1992). It is not known, however, if rate of fiber digestion can be altered through genetic selection or how selection for decreased fiber concentration or increased extent of digestion will affect fiber digestion rate.

Brown-midrib mutants of maize are characterized by low acid detergent lignin concentration and produce forage higher in fiber digestibility than normal maize genotypes (Lechtenberg et al., 1972). Recent work suggests that brown-midrib lignin has a lower degree of polymerization than normal lignin (Lam et al., 1996). Brown-midrib mutants have expressed faster fractional rates of in vitro fiber digestion than normal maize in some experiments (Muller et al., 1972) and had inconsistent effects on digestion rates in other studies (Thorstensson et al., 1992). Poor agronomic performance of maize hybrids possessing the brown-midrib trait has limited its use in the production of commercially available hybrids (Miller et al., 1983).

A key factor limiting the development of maize genotypes with improved digestion kinetics is the high resource requirement for analysis of digestion kinetics in vitro. Near infrared reflectance spectroscopy (NIRS) is a rapid method for predicting forage quality and has been used successfully to estimate fiber concentration and in vitro dry matter digestibility (Villalobos et al., 1991; Gabrielsen et al., 1988; Marten et al., 1988) of forage grasses. If NIRS equations could be developed that predict fiber digestion kinetics accurately, plant breeders could evaluate much larger populations than is possible with standard in vitro techniques. Additionally, determination of fiber digestion kinetics is extremely laborious because of the requirement that many time points be measured during the course of digestion. If selected times could substitute for conducting complete digestion studies with eight to 10 fermentation times, estimates of digestion kinetic parameters could be streamlined.

The objectives of this study were to: (i) evaluate a

Abbreviations: NDF, neutral detergent fiber; INDF, indigestible NDF concentration; NIRS, near infrared reflectance spectroscopy; DM, dry matter; LSD, least significant difference.

Table 1. Calibration and validation statistics for prediction of NDF kinetic variables of maize inbreds by NIRS.

Variable	*n*†	Mean	SEC‡	R^2§	SECV¶	1−VR#
Direct prediction of kinetic parameters						
NDF, g kg^{-1} DM	88	583	10	0.96	17	0.89
Rate, h^{-1}	89	0.061	0.001	0.56	0.013	0.35
INDF, g kg^{-1} DM	88	226	18	0.86	22	0.78
Extent, g kg^{-1} NDF	86	616	14	0.83	24	0.52
Lag, h	87	3	1	0.07	1	0.04
Prediction of residues at each fermentation time, g kg^{-1} DM						
0 h	88	583	10	0.96	17	0.89
3 h	88	572	11	0.95	17	0.90
6 h	85	533	10	0.97	19	0.89
9 h	83	482	19	0.90	22	0.86
12 h	80	437	18	0.92	33	0.72
18 h	84	377	21	0.89	26	0.84
24 h	84	333	26	0.84	30	0.78
36 h	81	281	17	0.92	23	0.85
48 h	78	261	17	0.90	21	0.85
72 h	84	237	16	0.89	20	0.84
96 h	88	225	17	0.88	21	0.82

† *n* = number of samples in calibration.
‡ SEC = standard error of calibration.
§ R2 = coefficient of determination.
¶ SECV = standard error of cross-validation.
# 1-VR = coefficient of determination for cross-validation.

diverse group of maize inbreds for differences in fiber concentration and digestion kinetic parameters of the lower internodes of the stalk, (ii) determine the relationships between fiber concentration and fiber digestion kinetics of stalk internodes, (iii) evaluate the use of NIRS for predicting fiber digestion kinetic parameters, and (iv) evaluate the use of selected times to estimate differences in digestion kinetics.

MATERIAL AND METHODS

Forty-five maize inbred lines were grown at the Iowa State Agronomy Research Farm west of Ames, IA, during 1989 and 1990 for use in this experiment. The experiment was conducted in a randomized block design with four field replicates per year. A detailed description of growing, harvesting, and processing procedures, plus a description of the genetic background of the inbreds, was presented by Lundvall et al. (1994). At 50% silking, the two lowest aboveground internodes were harvested from four plants from each replication, oven dried at 60°C, and ground to pass a 1-mm screen in a cyclone-type mill. Lower internodes were selected because they are the most intensively lignified internodes in corn (Morrison et al., 1994) and therefore may provide the greatest opportunity to detect differences among genotypes. It was assumed that drying samples would have no differential effects on the estimation of kinetic parameters among genotypes. Spectra from all samples were collected for NIRS analysis with a Pacific Scientific (Silver Springs, MD) Model 6250 scanning monochrometer with a range of 1100 to 2500 nm.

One field replicate of each inbred from each year was used for conventional in vitro analysis (90 samples). Samples were incubated at 39°C under constant CO_2 pressure using the in vitro procedure of Goering and Van Soest (1970). Residues were recovered after single incubations of 0, 3, 6, 9, 12, 18, 24, 36, 48, 72, or 96 h and analyzed for NDF by a modification of the technique described by Goering and Van Soest (1970). Modifications included elimination of decalin and the addition of 2 mL of a 2% solution of heat-stable α-amylase during refluxing.

The in vitro data were used to calculate digestion kinetic variables. Nonlinear regression techniques as described by Grant and Mertens (1992) were used to fit the residue data

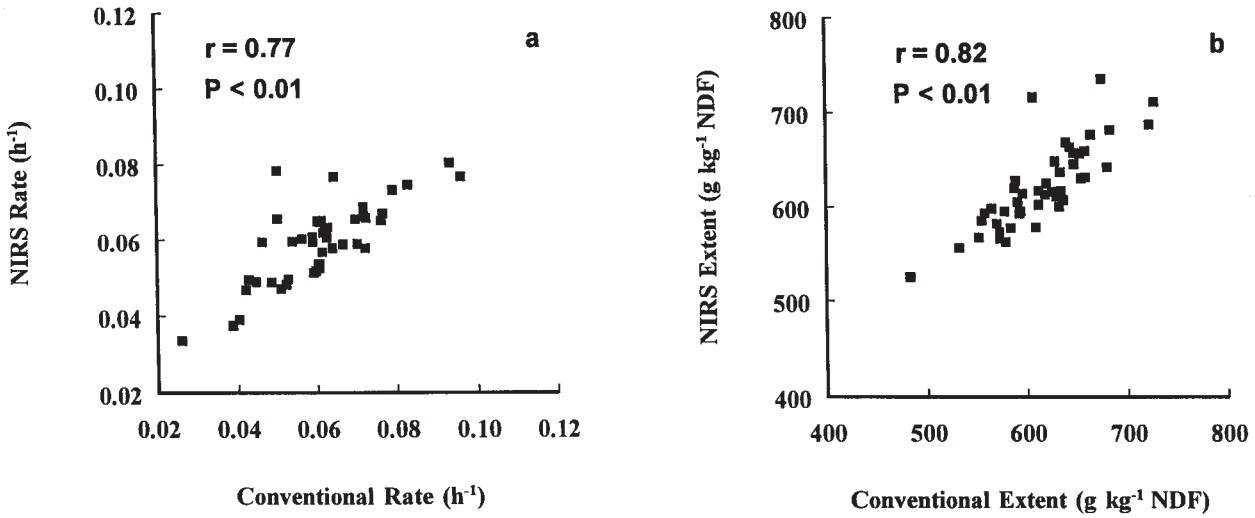

Fig. 1. Relationships between conventional analysis and NIRS data (calculated from predicted times) for rate of NDF digestion (a) and extent of NDF digestion (b) of 45 maize inbreds.

Table 2. Mean squares for NDF digestion kinetic parameters determined by conventional analysis of maize inbreds.

Source	df	NDF	Rate†	INDF	Extent	Lag
Year	1	35 129**	0.49	36 987**	45 350**	8.99*
Inbred	44	4 253**	0.37**	2 818**	4 666**	2.79
Error	44	818	0.13	686	1 492	1.81

*,** Significant at the 0.05 and 0.01 probability levels, respectively.
† Mean squares × 1000 for NDF digestion rate.

to the first-order model of Mertens (1973) in the form:

$$Y = D_0\, e^{[-Kd(t-L)]} + INDF$$

where Y = NDF residue at time t, D_0 = potentially digestible NDF (g kg^{-1} DM), Kd = fractional rate constant of digestion (h^{-1}), L = discrete lag (h), t = time (h), and INDF = asymptotic indigestible NDF (g kg^{-1} DM). Potential extent of digestion (g kg^{-1} NDF) was calculated as 1000 × (NDF−INDF)/NDF.

Near infrared spectroscopy calibration equations were developed for NDF concentration, NDF residue remaining at each of the individual fermentation times, and NDF digestion kinetic parameters (Kd, L, and INDF). Equations for NIRS prediction were developed using the Infrasoft International (ISI, Port Matilda, PA) NIRS 3 ver. 3.0 software program "Calibrate" with the modified partial least squares regression option and two passes to eliminate outliers (Shenk and Westerhaus, 1991). The math treatment of 1, 4, 4, 1 (first derivative, gap over which derivative was calculated, number of data points used in first smoothing, and no second smoothing) was used for all prediction equations (Table 1). Digestion kinetic parameters were estimated by NIRS using two different methods. One method involved directly predicting NDF digestion kinetic parameters for each sample. The second method involved predicting NDF residues for each sample at all 10 fermentation times used in the in vitro study and then calculating digestion kinetic parameters by fitting residues predicted by NIRS to the same kinetic model used for the in vitro data.

Values for NDF concentration and digestion kinetic parameters using in vitro data on one-quarter of the samples (conventional analysis data set) were statistically analyzed as a randomized complete block design using the entry × year interaction as the error term and years as replicates. The digestion kinetic parameters derived from NIRS predictions, both direct prediction and calculation from predicted times, were analyzed as a randomized complete block design repeated over 2 yr. Correlation analysis was done on the conventional and NIRS data sets across inbred means (n = 45). Procedures from the SAS statistical analysis package were used for all statistical analyses (SAS Institute, 1985).

RESULTS AND DISCUSSION

The NIRS prediction equations developed from conventional analysis of one-quarter of the maize inbred samples were of acceptable quality ($R^2 > 0.80$) for all traits examined, except direct prediction of NDF digestion rate and lag time (Table 1). The equation for direct prediction of NDF digestion rate only accounted for 56% of the variation in the conventional data set and direct prediction of lag accounted for almost none of the variation (7%) in the trait. We found good correlations (r = 0.77–0.92) between conventional analysis and the two NIRS prediction methods for NDF concentration and digestion kinetic parameters for the maize inbreds, but not for lag time (r = −0.23 and 0.55, conventional vs. NIRS direct and conventional vs. NIRS residues, respectively). Fisher et al. (1994) evaluated the ability of NIRS to predict in vitro digestion kinetics of switchgrass (*Panicum virgatum* L.) germplasms and reported that calculations based on NIRS estimates of residues at individual fermentation times were more closely related to measured values than were those directly predicted by NIRS. Agreement among the two NIRS methods for predicting digestion kinetics was good in our study except lag time. Correlation coefficients were 0.95, 0.99, and 0.99 for rate of fiber digestion, INDF concentration, and potential extent of NDF digestion, respectively. Kinetic parameters calculated from NIRS predicted residues at each fermentation time are emphasized from now on because direct prediction by NIRS was poor for lag time and marginal for a fractional rate of NDF digestion (Table 1). The relationships between conventional analysis and NIRS prediction for rate and potential extent of NDF digestion, calculated from predicted fermentation residues, are illustrated in Fig. 1.

Both in vitro analysis and NIRS predictions show that genetic variation exists among these 45 maize inbreds for fiber digestion kinetics. Significant variation among maize inbreds was detected for NDF concentration and all digestion kinetic parameters, except lag time, in the conventional analysis data set (Table 2). All fiber traits, including lag time, varied among inbreds for the two NIRS-based data sets (Table 3). Year effects were significant for most fiber traits in all three data sets and in the NIRS data sets, where the inbred × year interaction could be tested, significant variation due to this genotype × environment interaction was detected for all fiber traits. The presence of a significant genotype × year interaction agrees with the findings of Lundvall et al. (1994) for other measurements of forage quality in these 45 inbreds and suggests that accurate identification of inbred lines with superior digestion characteristics will require evaluations in multiple environments. Dhillon et al. (1990) and Argillier et al. (1995) have also reported significant genotype × environment interactions for forage quality traits in maize inbreds and hybrids.

The presence of genotype × environment interactions for forage quality may make breeding for improved quality in maize more difficult than in perennial forage species where such interactions are normally absent or small in magnitude (Buxton and Casler, 1993). However, significant genotype × environment interactions may exist in perennial forages as

Table 3. Mean squares for NDF digestion kinetic parameters directly predicted by NIRS and calculated from NIRS predicted fermentation residues of maize inbreds.

			Rate†		INDF		Extent		Lag	
Source	df	NDF	Direct‡	Calc	Direct	Calc	Direct	Calc	Direct	Calc
Year	1	121 797*	1.81	0.08	178 348**	172 123**	260 074**	254 004**	9.57*	6.54
Inbred	44	11 037**	0.83**	0.67**	8 437**	8 793**	13 931**	14 236**	0.12**	3.16**
Year* Inbred	44	1 672**	0.10**	0.11**	869**	1 047**	1 622**	2 032**	0.07**	1.06
Error	246	813	0.05	0.06	460	526	828	966	0.04	0.77

*,** Significant at the 0.05 and 0.01 probability levels, respectively.
† Mean squares × 1000 for NDF digestion rate.
‡ Direct = direct NIRS prediction of kinetic trait; Calc = kinetic trait calculated from NIRS predicted fermentation residues.

suggested in work with smooth bromegrass (*Bromus inermis* Leyss.) clones (Casler et al., 1987). The smaller impact of genotype × environment interactions generally observed in studies of perennial forages may be a reflection of the heterozygous and polyploid nature of most perennial forages due to obligate out-crossing.

Because they are based on regression equations, NIRS predictions narrowed the range of the kinetic parameters compared to conventional in vitro methods. Using the conventional analysis data set (n = 90), predicted concentration of NDF in the inbreds ranged from 478 to 651 g kg^{-1} DM. By comparison, the range for conventionally measured NDF among the inbreds was 466 to 700 g kg^{-1} DM. There was a twofold range in fractional rate of NDF digestion determined by NIRS (0.037–0.080 h^{-1}) compared with a threefold range from in vitro data (0.026–0.096 h^{-1}). Indigestible NDF ranged from 147 to 301 g kg^{-1} DM for NIRS prediction compared with 139 to 322 g kg^{-1} for conventional analysis. Potential extent of NDF digestion varied greatly among the inbreds for both NIRS (516–722 g kg^{-1} NDF) and conventional analysis (484–726 g kg^{-1} NDF). The narrower range of NIRS predictions suggests that it may be more difficult to detect differences among genotypes using NIRS compared to reference analysis when a similar number of replications are used. However, the ease of NIRS analysis allows more replications to be analyzed while using fewer resources.

Table 4. Neutral detergent fiber concentration and digestion kinetics of maize inbreds calculated from NIRS predicted fermentation residues.

Inbred	NDF	Rate	INDF	Extent	Lag
	g kg^{-1} DM	h^{-1}	g kg^{-1} DM	g kg^{-1} NDF	h
B14A	638	0.049	277	567	2.39
B14Ao2	662	0.037	246	628	0.53
B37	608	0.056	240	607	2.87
B52	643	0.040	272	577	1.34
B57	538	0.063	157	711	2.32
B64	618	0.037	270	566	2.31
B68	651	0.048	251	617	2.25
B73	584	0.061	248	578	2.94
B73o2	558	0.074	183	676	3.48
B75	604	0.050	268	556	2.40
B76	573	0.060	223	613	3.41
B77	513	0.073	166	681	3.19
B78	564	0.064	206	637	2.93
B79	628	0.061	276	562	2.24
B84	588	0.059	239	595	3.40
B86	546	0.042	229	582	1.35
B87	590	0.055	205	657	1.82
B88	606	0.054	236	611	2.33
B89	636	0.047	254	600	1.84
B90	612	0.054	227	631	1.96
B91	592	0.056	206	656	2.14
B93	546	0.058	211	616	2.28
B94	585	0.055	218	630	2.70
bm1bm1	544	0.069	147	735	2.87
bm2bm2	510	0.063	148	716	2.04
BS16(V)C2-1bm	579	0.051	238	593	2.28
L289	633	0.045	258	596	1.71
L317	519	0.064	222	573	3.16
LAN232	578	0.060	192	668	2.80
LAN496	622	0.045	296	525	1.57
MO17	574	0.071	194	663	3.77
N7A	603	0.054	219	642	2.00
NC252	576	0.062	217	625	2.83
NC254	576	0.055	205	648	2.26
NC256	590	0.059	245	585	3.51
NC258	587	0.062	184	687	2.22
NC262	606	0.051	240	605	2.66
NC264	578	0.062	206	645	2.24
NC266	593	0.062	240	598	2.68
NC268	578	0.058	231	602	2.95
NC270	593	0.060	243	593	2.92
NC272	556	0.054	214	617	2.02
R225	544	0.071	211	614	2.71
R226	550	0.067	211	620	2.89
R227	497	0.077	171	659	3.06
LSD (0.05)	29	0.008	23	31	0.88
Mean	584	0.057	223	621	2.48
Minimum	497	0.037	147	525	0.53
Maximum	662	0.077	296	735	3.77

Maize inbred means for NDF concentration and digestion kinetics calculated from NIRS predicted residues represent four replications per year for 2 yr (Table 4), whereas only one replicate for each year was analyzed by conventional in vitro analysis. Even though there was generally good agreement between conventional and NIRS predicted kinetic parameters of fiber digestion (rank correlations exceeding 0.93), typically only seven of the 10 genotypes identified as superior by either method would be identified by the other. Buxton and Mertens (1991) found that significant bias can exist in NIRS generated data and suggested caution in the use of NIRS for detecting differences. They recommended that NIRS be used as a screening tool during breeding studies and that the selected subset of genotypes be verified by conventional analysis.

Inbreds within the LSD of the smallest NDF or INDF concentrations or largest fractional rate constant or potential extent of digestion were defined as a statistically similar group having the highest quality for each variable. The NIRS results show that inbreds R227 and B77 were in the groups with the lowest NDF concentration and fastest rate of digestion. In addition, inbred B77 was in the group with the lowest INDF concentration. Brown-midrib inbred bm2bm2 also had low NDF and INDF concentrations and high potential extent of digestion. Based on conventual analysis, inbreds R227 and bm2bm2 were in the highest quality group for NDF concentration and rate of fiber digestion and R227 was also in the group with the lowest INDF concentration. Inbred B77 was in the groups with fastest rate, lowest INDF concentration, and highest potential extent of digestion. Brown-midrib bm1bm1 was in the group with the highest rate and lowest INDF concentration.

Brown-midrib maize is commonly assumed to be superior to isogenic normal types for digestibility (Barriere and Argillier, 1993). We did not have the normal isogenic lines for these three brown-midrib inbreds in this study. Normal inbreds were identified in our study that equaled or exceeded the brown-midrib inbreds for every NDF digestion kinetic trait. One brown-midrib inbred (BS16(V)C2-1bm) in the experiment was of only average quality for all fiber traits. The identification of normal inbreds with NDF concentration, rate of NDF digestion, and extent of NDF digestion values equal to or superior to brown-midrib inbreds shows that it should be possible to improve the digestibility of maize stalks by selection within agronomically superior inbreds and not require the incorporation of undesirable agronomic characteristics associated with the brown-midrib trait, as has been previously sug-

Table 5. Correlations of rate and extent of NDF digestion with NDF digestibility at each of the times used in the kinetics analysis. Data are from the conventional analysis.

Fermentation time	Rate of NDF digestion	Extent of NDF digestion
3 h	−0.16	0.13
6 h	0.13	0.36*
9 h	0.56**	0.52**
12 h	0.72**	0.42**
18 h	0.79**	0.61**
24 h	0.64**	0.61**
36 h	0.70**	0.73**
48 h	0.53**	0.84**
72 h	0.51**	0.90**
96 h	0.49**	0.96**

*,** Significant at the 0.05, and 0.01 probability level, respectively.

gested by Miller et al. (1983). However, more recent research shows that much of the negative agronomic behavior of the brown-midrib trait can be overcome through use of the correct genetic background (Gentinetta et al., 1990).

In comparing our results with previous reports, it must be remembered that our data were obtained from maize plants at an immature stage of development (silking), whereas most other data are from maize at a maturity stage typical for silage production (near physiological maturity). Lundvall et al. (1994) showed that the range for forage quality traits among inbreds increased with maturity. The range in stalk NDF concentration observed in this study is still greater than that previously reported for inbred lines (Albrecht et al., 1986) or hybrids (Albrecht et al., 1986; Bures et al., 1992; Hunt et al., 1992), and is of sufficient magnitude to affect the quantity of forage consumed by ruminant animals (Mertens, 1985). We know of no other published data on variation among maize inbreds for rate of NDF digestion. Casler et al. (1987) reported significant differences in rate of NDF digestion among smooth bromegrass clones that ranged from 0.049 to 0.065 h^{-1}. The range in rate of NDF digestion among the maize inbreds in this study was much greater and can be expected to markedly affect animal performance. Just as for rate, there are no other maize data for comparing extent of NDF digestion. Digestibility of NDF after 48-h fermentations ranged from 420 to 605 g kg^{-1} NDF among a set of 44 maize hybrids (Dolstra et al., 1987). This observed range is of similar magnitude to that for extent of NDF digestion of the 45 inbreds we examined.

Even though NIRS use can significantly reduce the time and resources needed for estimating NDF digestion kinetic parameters in breeding studies, NIRS calibration still requires conducting eight to 10 time point fermentations by conventional analytical methods for each sample in the calibration set. We examined the correlations of rate and extent of NDF digestion with digestibility of NDF at each of the times employed in our study as an additional way to reduce the number of in vitro fermentations that need to be done in ranking entries in breeding studies. Digestibility of NDF at all fermentation times, except the 3- and 6-h intervals, was significantly correlated with rate and extent of NDF digestion (Table 5). As expected, 96-h NDF digestibility was most highly correlated with potential extent of digestion. The situation for rate of digestion was less clear. The fermentation intervals from 12- to 36-h all had similar correlations of NDF digestibility with rate of digestion. The ranking of inbreds based on individual time point NDF digestibilities vs. actual determination of rate and extent of NDF digestion is illustrated in Fig. 2. The two highest ranking inbreds for 18-h NDF digestibility were also the two with the highest rate of NDF digestion. Inbreds with the third and fourth highest 18-h digestibility inbreds were ranked much lower based on actual rate of digestion, but the fifth highest inbred was the same by both methods. While none of the inbreds ranked the same for 96-h NDF digestibility and extent of NDF digestion, the differences in inbred ranking by these methods was small.

Table 6. Correlations among NDF concentration and digestion kinetic parameters of maize inbreds.‡

Trait	NDF	Rate	INDF	Potential extent	Lag
NDF	–	−0.53**	0.69**	−0.31*	−0.19
Rate	−0.76**	–	−0.46**	0.28†	0.50**
INDF	0.75**	−0.65**	–	−0.90**	−0.18
Extent	−0.44**	0.44**	−0.92**	–	0.11
Lag	0.18	−0.22	0.23	−0.19	–

†,*,** Significant at the 0.10, 0.05, and 0.01 probability level, respectively.
‡ Values above the diagonal are for conventional analysis data and values below the diagonal are for NIRS data (n = 45).

Significant correlations were observed among the fiber digestion parameters measured (Table 6). Concentration of NDF was negatively correlated with both rate of NDF digestion and potential extent of NDF digestion. Rate of NDF digestion was positively correlated with potential extent of NDF digestion. And the observed correlations among these traits were generally similar in the NIRS and conventional analysis data sets. In contrast to the correlations between rate of NDF digestion and extent of NDF digestion in the NIRS data sets, Jung and Buxton (1994) reported almost no correlations between 24- and 96-h in vitro cell-wall neutral sugar degradabilities for these 45 inbreds. This result is more in agreement with the conventional analysis results (Table 6). However, even for the NIRS data sets the correlations accounted for little of the variation between rate and extent of NDF digestion. This suggests that factors regulating rate of NDF digestion are at least partially independent of the factors regulating extent of NDF digestion.

Our data show that there is significant genetic variation for fiber digestion kinetics of maize stalks and that inbred lines from normal populations can provide variation equal to

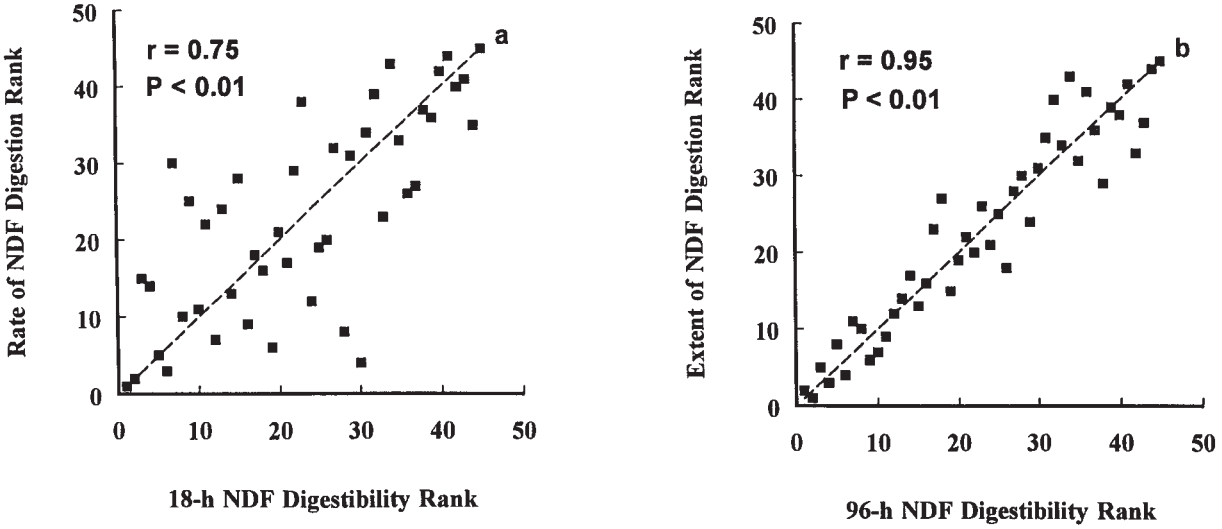

Fig. 2. Maize inbred ranking comparisons based on (a) 18-h NDF digestibility vs. rate of NDF digestion and (b) 96-h NDF digestibility vs. extent of NDF digestion. The diagonal line represents unity of the rankings.

brown-midrib mutants. Depending on the heritability of these traits and the impact that heterosis has on the progeny of superior inbred lines, it may be possible to improve genetically the fiber digestibility of maize hybrids. Correlations among the forage fiber quality traits appear small enough that progress for all three quality goals (low fiber, rapid fiber digestion, and highly digestible fiber) may be possible simultaneously. Near infrared reflectance spectroscopy can serve as an important screening tool in the selection process, but conventional analysis should be used to verify high-ranking genotypes. Single short (12- to 36-h) and long (96-h) fermentations may also serve as a more rapid screening procedure for identifying lines with rapid rates and high extents of fiber digestion, respectively.

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